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DEC 18 2001

TECH CENTER 1600/2900

DATE: 12/05/2001  
TIME: 10:30:46

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/842,347A  
Input Set : N:\Crf3\RULE60\09842347A.txt  
Output Set: N:\CRF3\12052001\I842347A.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: TAKAHASHI, Tohru  
7 SERIZAWA, Nobufusa  
8 KOISHI, Ryuta  
9 KAWASHIMA, Ichiro

11 (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING  
12 AUTOLYZING FUSION PROTEINS  
13 AND A NOVEL REDUCING POLYPEPTIDE

15 (iii) NUMBER OF SEQUENCES: 19

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.  
19 (B) STREET: 767 Third Avenue-25th Floor  
20 (C) CITY: New York  
21 (D) STATE: New York  
22 (E) COUNTRY: United States  
23 (F) ZIP: 10017-2023

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk  
27 (B) COMPUTER: IBM PC compatible  
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
29 (D) SOFTWARE: PatentIn Release #1.24

31 (vi) CURRENT APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/09/842,347A  
C--> 33 (B) FILING DATE: 25-Apr-2001  
34 (C) CLASSIFICATION:

43 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/500,635  
38 (B) FILING DATE: 1995-07-11  
40 (A) APPLICATION NUMBER: JP 6-218392  
41 (B) FILING DATE: 13-SEP-1994  
44 (A) APPLICATION NUMBER: JP 6-303809  
45 (B) FILING DATE: 07-DEC-1994

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: Goodman, Herbert  
49 (B) REGISTRATION NUMBER: 17081  
50 (C) REFERENCE/DOCKET NUMBER: 950376/HG

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: (212) 319-4900  
54 (B) TELEFAX: (212) 319-5101  
55 (C) TELEX: 236268

58 (2) INFORMATION FOR SEQ ID NO: 1:

60 (i) SEQUENCE CHARACTERISTICS:

61 (A) LENGTH: 1320 base pairs  
62 (B) TYPE: nucleic acid  
63 (C) STRANDEDNESS: double  
64 (D) TOPOLOGY: linear

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66 (ii) MOLECULE TYPE: cDNA to mRNA  
 W--> 68 (iii) HYPOTHETICAL: N  
 W--> 70 (iv) ANTI-SENSE: N  
 72 (vi) ORIGINAL SOURCE:  
 73 (A) ORGANISM: Clover Yellow Vein Virus  
 75 (ix) FEATURE:  
 76 (A) NAME/KEY: CDS  
 77 (B) LOCATION: 1..1320  
 78 (D) OTHER INFORMATION:  
 79 (ix) FEATURE:  
 80 (A) NAME/KEY: mat\_peptide  
 81 (B) LOCATION: 10..1311  
 82 (D) OTHER INFORMATION:  
 86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 88 AAG TTC CAA GGG AAA AGT AAG AGA ACA AGA CAA AAG TTG AAG TTC AGA 48  
 89 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg  
 90 1 5 10 15  
 92 GCG GCA AGA GAC ATG AAG GAT CGT TAT GAA GTG CAT GCC GAT GAG GGG 96  
 93 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly  
 94 20 25 30  
 96 ACT TTA GTG GAA AAT TTT GGA ACT CGT TAT TCA AAG AAA GGC AAG ACA 144  
 97 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr  
 98 35 40 45  
 100 AAA GGT ACT GTT GTG GGT TTG GGT GCA AAA ACA AGA CGG TTC ACT AAC 192  
 101 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn  
 102 50 55 60  
 104 ATG TAT GGT TTT GAC CCC ACG GAG TAT TCA TTT GCT AGG TAT CTT GAT 240  
 105 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp  
 106 65 70 75 80  
 108 CCA ATC ACG GGT GCA ACA TTG GAT GAA ACC CCA ATT CAC AAT GTA AAT 288  
 109 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn  
 110 85 90 95  
 112 TTG GTT GCT GAG CAT TTT GGC GAC ATA AGG CTT GAT ATG GTT GAC AAG 336  
 113 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys  
 W--> 114 100 105 110  
 116 GAG TTA CTT GAC AAA CAG CAC TTA TAC CTC AAG AGA CCA ATA GAA TGT 384  
 117 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys  
 W--> 118 115 120 125  
 120 TAC TTT GTA AAG GAT GCT GGT CAG AAG GTG ATG AGG ATT GAT CTA ACA 432  
 121 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr  
 W--> 122 130 135 140  
 124 CCC CAC AAC CCA TTG TTG GCA AGC GAT GTT AGC ACA ACC ATA ATG GGT 480  
 125 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly  
 W--> 126 145 150 155 160  
 128 TAT CCT GAG AGA GAA GGT GAA CTC CGT CAA ACT GGA AAG GCA AGG TTA 528  
 129 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu  
 W--> 130 165 170 175  
 132 GTC GAC CCA TCA GAG TTG CCC GCG CGG AAT GAG GAT ATT GAT GCA GAG 576  
 133 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu

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W--> 134	180	185	190	
136	TTT GAG AGT CTA AAT CGC ATA AGT GGT TTG CGC GAC TAT AAT CCC ATT			624
137	Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile			
W--> 138	195	200	205	
140	TCA CAA AAT GTT TGC TTG CTA ACA AAT GAG TCA GAA GGC CAT AGA GAG			672
141	Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Gly His Arg Glu			
W--> 142	210	215	220	
144	AAG ATG TTT GGA ATT GGA TAT GGT TCA GTG ATC ATT ACA AAT CAA CAT			720
145	Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His			
W--> 146	225	230	235	240
148	CTG TTC AGA AGG AAT AAT GGG GAG TTA TCA ATT CAA TCC AAG CAT GGC			768
149	Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly			
W--> 150	245	250	255	
152	TAC TTC AGA TGC CGC AAC ACC ACA AGC TTG AAG ATG CTG CCT TTG GAG			816
153	Tyr Phe Arg Cys Arg Asn Thr Ser Leu Lys Met Leu Pro Leu Glu			
W--> 154	260	265	270	
156	GGA CAT GAC ATT TTG TTG ATT CAG TTA CCA AGG GAC TTT CCA GTG TTT			864
157	Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe			
W--> 158	275	280	285	
160	CCA CAA AAG ATT CGC TTT AGG GAG CCA AGA GTG GAT GAC AAA ATT GTT			912
161	Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val			
W--> 162	290	295	300	
164	TTG GTC AGC ACA AAT TTC CAG GAA AAG AGT TCC TCG AGC ACG GTC TCA			960
165	Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Thr Val Ser			
W--> 166	305	310	315	320
168	GAG TCC AGT AAC ATT TCA AGA GTG CAG TCA GCC AAT TTC TAC AAG CAT			1008
169	Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His			
W--> 170	325	330	335	
172	TGG ATC TCA ACA GTA GCA GGA CAC TGT GGA AAC CCT ATG GTT TCG ACT			1056
173	Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr			
W--> 174	340	345	350	
176	AAA GAT GGA TTT ATT GTA GGT ATC CAC AGT CTT GCT TCA TTG ACA GGC			1104
177	Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly			
W--> 178	355	360	365	
180	GAC GTT AAC ATC TTC ACA AGC TTT CCG CCG CAG TTT GAG AAC AAA TAT			1152
181	Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr			
W--> 182	370	375	380	
184	CTA CAG AAG CTC AGT GAA CAC ACA TGG TGT AGT GGA TGG AAA CTA AAT			1200
185	Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn			
W--> 186	385	390	395	400
188	CTT GGA AAG ATT AGT TGG GGT GGA ATC AAC ATT GTG GAG GAT GCA CCT			1248
189	Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro			
W--> 190	405	410	415	
192	GAA GAG CCC TTT ATA ACA TCC AAG ATG GCA AGC CTT CTT AGT GAT TTG			1296
193	Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu			
W--> 194	420	425	430	
196	AAT TGT TCA TTC CAA GCA AGT GCG			1320
197	Asn Cys Ser Phe Gln Ala Ser Ala			
W--> 198	435	440		

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201 (2) INFORMATION FOR SEQ ID NO: 2:  
203 (i) SEQUENCE CHARACTERISTICS:  
204 (A) LENGTH: 440 amino acids  
205 (B) TYPE: amino acid  
206 (D) TOPOLOGY: linear  
208 (ii) MOLECULE TYPE: protein  
210 (vi) ORIGINAL SOURCE:  
211 (A) ORGANISM: Clover Yellow Vein Virus  
213 (ix) FEATURE:  
214 (A) NAME/KEY: mat\_peptide  
215 (B) LOCATION: 4..437  
216 (D) OTHER INFORMATION:  
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
221 Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg  
222 1 5 10 15  
224 Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly  
225 20 25 30  
227 Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr  
228 35 40 45  
230 Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn  
231 50 55 60  
233 Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp  
234 65 70 75 80  
236 Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn  
237 85 90 95  
239 Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys  
240 100 105 110  
242 Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys  
243 115 120 125  
245 Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr  
246 130 135 140  
248 Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly  
249 145 150 155 160  
251 Tyr Pro Glu Arg Glu Gly Glu Leu Arg Gln Thr Gly Lys Ala Arg Leu  
252 165 170 175  
254 Val Asp Pro Ser Glu Leu Pro Ala Arg Asn Glu Asp Ile Asp Ala Glu  
255 180 185 190  
257 Phe Glu Ser Leu Asn Arg Ile Ser Gly Leu Arg Asp Tyr Asn Pro Ile  
258 195 200 205  
260 Ser Gln Asn Val Cys Leu Leu Thr Asn Glu Ser Glu Gly His Arg Glu  
261 210 215 220  
263 Lys Met Phe Gly Ile Gly Tyr Gly Ser Val Ile Ile Thr Asn Gln His  
264 225 230 235 240  
266 Leu Phe Arg Arg Asn Asn Gly Glu Leu Ser Ile Gln Ser Lys His Gly  
267 245 250 255  
269 Tyr Phe Arg Cys Arg Asn Thr Thr Ser Leu Lys Met Leu Pro Leu Glu  
270 260 265 270  
272 Gly His Asp Ile Leu Leu Ile Gln Leu Pro Arg Asp Phe Pro Val Phe  
273 275 280 285

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275 Pro Gln Lys Ile Arg Phe Arg Glu Pro Arg Val Asp Asp Lys Ile Val  
276 290 295 300  
278 Leu Val Ser Thr Asn Phe Gln Glu Lys Ser Ser Ser Ser Thr Val Ser  
279 305 310 315 320  
281 Glu Ser Ser Asn Ile Ser Arg Val Gln Ser Ala Asn Phe Tyr Lys His  
282 325 330 335  
284 Trp Ile Ser Thr Val Ala Gly His Cys Gly Asn Pro Met Val Ser Thr  
285 340 345 350  
287 Lys Asp Gly Phe Ile Val Gly Ile His Ser Leu Ala Ser Leu Thr Gly  
288 355 360 365  
290 Asp Val Asn Ile Phe Thr Ser Phe Pro Pro Gln Phe Glu Asn Lys Tyr  
291 370 375 380  
293 Leu Gln Lys Leu Ser Glu His Thr Trp Cys Ser Gly Trp Lys Leu Asn  
294 385 390 395 400  
296 Leu Gly Lys Ile Ser Trp Gly Gly Ile Asn Ile Val Glu Asp Ala Pro  
297 405 410 415  
299 Glu Glu Pro Phe Ile Thr Ser Lys Met Ala Ser Leu Leu Ser Asp Leu  
300 420 425 430  
302 Asn Cys Ser Phe Gln Ala Ser Ala  
303 435 440  
305 (2) INFORMATION FOR SEQ ID NO: 3:  
307 (i) SEQUENCE CHARACTERISTICS:  
308 (A) LENGTH: 25 base pairs  
309 (B) TYPE: nucleic acid  
310 (C) STRANDEDNESS: single  
311 (D) TOPOLOGY: linear  
313 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
W--> 315 (iii) HYPOTHETICAL: N 25  
W--> 317 (iv) ANTI-SENSE: N  
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
323 GTCCATGGGG AAAAGTAAGA GAACA

325 (2) INFORMATION FOR SEQ ID NO: 4:  
327 (i) SEQUENCE CHARACTERISTICS:  
328 (A) LENGTH: 20 base pairs  
329 (B) TYPE: nucleic acid  
330 (C) STRANDEDNESS: single  
331 (D) TOPOLOGY: linear  
333 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
W--> 335 (iii) HYPOTHETICAL: N 20  
W--> 337 (iv) ANTI-SENSE: N  
341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
343 ACTCTGAGAC CGTGCTCGAG  
345 (2) INFORMATION FOR SEQ ID NO: 5:  
347 (i) SEQUENCE CHARACTERISTICS:  
348 (A) LENGTH: 20 base pairs  
349 (B) TYPE: nucleic acid  
350 (C) STRANDEDNESS: single  
351 (D) TOPOLOGY: linear  
353 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/842,347A

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Input Set : N:\Crf3\RULE60\09842347A.txt  
Output Set: N:\CRF3\12052001\I842347A.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:68 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1  
L:70 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1  
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:315 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3  
L:317 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3  
L:335 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=4  
L:337 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=4  
L:355 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5  
L:357 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5  
L:375 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=6  
L:377 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=6  
L:395 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7  
L:397 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7  
L:415 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=8  
L:417 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=8  
L:435 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9  
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=10  
L:473 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11  
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11  
L:768 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13  
L:770 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13  
L:788 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=14  
L:790 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=14  
L:810 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15  
L:812 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15

## VERIFICATION SUMMARY

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L:830 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=16  
L:832 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=16  
L:850 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=17  
L:852 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=17  
L:870 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=18  
L:872 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=18  
L:893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19